SEQUENCE LISTING

<110> Lukyanov, Sergey

<120> Nucleic Acids Encoding Linked
Chromo/Fluorescent Domains and Methods for Using the Same

<130> CLON-094

<140> us 10/806,930
<141> 2004-03-22

<150> 09/976,673
<151> 2001-10-12

<150> 60/356,225
<151> 2002-02-11

<150> 60/383,336
<151> 2002-05-22

<150> PCT/US02/32560
<151> 2002-10-10

<160> 15

<170> FastSEQ for Windows Version 4.0

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cgccggcacc cagagcatgc ggatccacgt gaccgagggc gccccctgc ccttcgcctt 180
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caagagcggc ggctgggagc ccagcaccga ggtggtgtac cccgagaacg gcgtgctgtg 480
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cagctaccgg agcaagaagg ccgtgcgggc cctgaccatg cccggcttcc acttcaccga 600
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<210> 2
<211> 460
<212> PRT
<213> Anthozoa

<400> 2

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            20                  25                  30
Gly Asn Pro Phe Ala Gly Thr Gln Ser Met Arg Ile His Val Thr Glu
        35                  40                  45
Gly Ala Pro Leu Pro Phe Ala Phe Asp Ile Leu Ala Pro Cys Cys Glu
    50                  55                  60
Tyr Gly Ser Arg Thr Phe Val His His Thr Ala Glu Ile Pro Asp Phe
65                  70                  75                  80
Phe Lys Gln Ser Phe Pro Glu Gly Phe Thr Trp Glu Arg Thr Thr Thr
                85                  90                  95
Tyr Glu Asp Gly Gly Ile Leu Thr Ala His Gln Asp Thr Ser Leu Glu
            100                 105                 110
Gly Asn Cys Leu Ile Tyr Lys Val Lys Val Leu Gly Thr Asn Phe Pro
        115                 120                 125
Ala Asp Gly Pro Val Met Lys Asn Lys Ser Gly Gly Trp Glu Pro Ser
    130                 135                 140
Thr Glu Val Val Tyr Pro Glu Asn Gly Val Leu Cys Gly Arg Asn Val
145                 150                 155                 160
Met Ala Leu Lys Val Gly Asp Arg Arg Leu Ile Cys His His Tyr Thr
                165                 170                 175
Ser Tyr Arg Ser Lys Lys Ala Val Arg Ala Leu Thr Met Pro Gly Phe
            180                 185                 190
His Phe Thr Asp Ile Arg Leu Gln Met Leu Arg Lys Glu Lys Asp Glu
        195                 200                 205
Tyr Phe Glu Leu Tyr Glu Ala Ser Val Ala Arg Tyr Ser Asp Leu Pro
    210                 215                 220
Glu Lys Ala Asn Arg Ser Pro Gly Met Val Ser Gly Leu Leu Lys Glu
225                 230                 235                 240
Ser Met Arg Ile Lys Met Tyr Met Glu Gly Thr Val Asn Gly His Tyr
                245                 250                 255
Phe Lys Cys Glu Gly Glu Gly Asp Gly Asn Pro Phe Ala Gly Thr Gln
            260                 265                 270
Ser Met Arg Ile His Val Thr Glu Gly Ala Pro Leu Pro Phe Ala Phe
        275                 280                 285
Asp Ile Leu Ala Pro Cys Cys Glu Tyr Gly Ser Arg Thr Phe Val His
    290                 295                 300
His Thr Ala Glu Ile Pro Asp Phe Phe Lys Gln Ser Phe Pro Glu Gly
305                 310                 315                 320
Phe Thr Trp Glu Arg Thr Thr Thr Tyr Glu Asp Gly Gly Ile Leu Thr
                325                 330                 335
Ala His Gln Asp Thr Ser Leu Glu Gly Asn Cys Leu Ile Tyr Lys Val
            340                 345                 350
Lys Val Leu Gly Thr Asn Phe Pro Ala Asp Gly Pro Val Met Lys Asn
        355                 360                 365
Lys Ser Gly Gly Trp Glu Pro Ser Thr Glu Val Val Tyr Pro Glu Asn
    370                 375                 380
Gly Val Leu Cys Gly Arg Asn Val Met Ala Leu Lys Val Gly Asp Arg
385                 390                 395                 400
Arg Leu Ile Cys His His Tyr Thr Ser Tyr Arg Ser Lys Lys Ala Val
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                405                 410                 415
Arg Ala Leu Thr Met Pro Gly Phe His Phe Thr Asp Ile Arg Leu Gln
            420                 425                 430
Met Leu Arg Lys Glu Lys Asp Glu Tyr Phe Glu Leu Tyr Glu Ala Ser
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Val Ala Arg Tyr Ser Asp Leu Pro Glu Lys Ala Asn
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<210> 3
<211> 1424
<212> DNA
<213> Anthozoa

<400> 3

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cgccggcacc cagagcatgc ggatccacgt gaccgagggc gccccctgc ccttcgcctt 180
cgacatcctg gccccctgct gcgagtacgg cagcaggacc ttcgtgcacc acaccgccga 240
gatccccgac ttcttcaagc agagcttccc cgagggcttc acctgggaga gaaccaccac 300
ctacgaggac ggcggcatcc tgaccgccca ccaggacacc agcctggagg gcaactgcct 360
gatctacaag gtgaaggtgc tgggcaccaa cttccccgcc gacggccccg tgatgaagaa 420
caagagcggc ggctgggagc ccagcaccga ggtggtgtac cccgagaacg gcgtgctgtg 480
cggccggaac gtgatggccc tgaaggtggg cgaccggcgg ctgatctgcc accactacac 540
cagctaccgg agcaagaagg ccgtgcgggc cctgaccatg cccggcttcc acttcaccga 600
catccggctg cagatgctgc ggaaggagaa ggacgagtac ttcgagctgt acgaggccag 660
cgtggcccgg tacagcgacc tgcccgagaa ggccaacaga tctcccggga tggtgagcgg 720
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cttcaagtgc gagggcgagg gcgacggcaa ccccttcgcc ggcacccaga gcatgcggat 840
ccacgtgacc gagggcgccc ccctgccctt cgccttcgac atcctggccc cctgctgcga 900
gtacggcagc aggaccttcg tgcaccacac cgccgagatc cccgacttct tcaagcagag 960
cttccccgag ggcttcacct gggagagaac caccacctac gaggacggcg gcatcctgac 1020
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caccaacttc cccgccgacg gccccgtgat gaagaacaag agcggcggct gggagcccag 1140
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gcgggccctg accatgcccg gcttccactt caccgacatc cggctgcaga tgctgcggaa 1320
ggagaaggac gagtacttcg agctgtacga ggccagcgtg gcccggtaca gcgacctgcc 1380
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<210> 4
<211> 470
<212> PRT
<213> Anthozoa

<400> 4

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            20                  25                  30
Gly Asn Pro Phe Ala Gly Thr Gln Ser Met Arg Ile His Val Thr Glu
        35                  40                  45
Gly Ala Pro Leu Pro Phe Ala Phe Asp Ile Leu Ala Pro Cys Cys Glu
    50                  55                  60
Tyr Gly Ser Arg Thr Phe Val His His Thr Ala Glu Ile Pro Asp Phe
65                  70                  75                  80
Phe Lys Gln Ser Phe Pro Glu Gly Phe Thr Trp Glu Arg Thr Thr Thr
                85                  90                  95
Tyr Glu Asp Gly Gly Ile Leu Thr Ala His Gln Asp Thr Ser Leu Glu
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```
            100                 105                 110
Gly Asn Cys Leu Ile Tyr Lys Val Lys Val Leu Gly Thr Asn Phe Pro
        115                 120                 125
Ala Asp Gly Pro Val Met Lys Asn Lys Ser Gly Gly Trp Glu Pro Ser
    130                 135                 140
Thr Glu Val Val Tyr Pro Glu Asn Gly Val Leu Cys Gly Arg Asn Val
145                 150                 155                 160
Met Ala Leu Lys Val Gly Asp Arg Arg Leu Ile Cys His His Tyr Thr
                165                 170                 175
Ser Tyr Arg Ser Lys Lys Ala Val Arg Ala Leu Thr Met Pro Gly Phe
            180                 185                 190
His Phe Thr Asp Ile Arg Leu Gln Met Leu Arg Lys Glu Lys Asp Glu
        195                 200                 205
Tyr Phe Glu Leu Tyr Glu Ala Ser Val Ala Arg Tyr Ser Asp Leu Pro
    210                 215                 220
Glu Lys Ala Asn Arg Ser Pro Gly Met Val Ser Gly Leu Leu Lys Glu
225                 230                 235                 240
Ser Met Arg Ile Lys Met Tyr Met Glu Gly Thr Val Asn Gly His Tyr
                245                 250                 255
Phe Lys Cys Glu Gly Glu Gly Asp Gly Asn Pro Phe Ala Gly Thr Gln
            260                 265                 270
Ser Met Arg Ile His Val Thr Glu Gly Ala Pro Leu Pro Phe Ala Phe
        275                 280                 285
Asp Ile Leu Ala Pro Cys Cys Glu Tyr Gly Ser Arg Thr Phe Val His
    290                 295                 300
His Thr Ala Glu Ile Pro Asp Phe Phe Lys Gln Ser Phe Pro Glu Gly
305                 310                 315                 320
Phe Thr Trp Glu Arg Thr Thr Thr Tyr Glu Asp Gly Gly Ile Leu Thr
                325                 330                 335
Ala His Gln Asp Thr Ser Leu Glu Gly Asn Cys Leu Ile Tyr Lys Val
            340                 345                 350
Lys Val Leu Gly Thr Asn Phe Pro Ala Asp Gly Pro Val Met Lys Asn
        355                 360                 365
Lys Ser Gly Gly Trp Glu Pro Ser Thr Glu Val Val Tyr Pro Glu Asn
    370                 375                 380
Gly Val Leu Cys Gly Arg Asn Val Met Ala Leu Lys Val Gly Asp Arg
385                 390                 395                 400
Arg Leu Ile Cys His His Tyr Thr Ser Tyr Arg Ser Lys Lys Ala Val
                405                 410                 415
Arg Ala Leu Thr Met Pro Gly Phe His Phe Thr Asp Ile Arg Leu Gln
            420                 425                 430
Met Leu Arg Lys Glu Lys Asp Glu Tyr Phe Glu Leu Tyr Glu Ala Ser
        435                 440                 445
Val Ala Arg Tyr Ser Asp Leu Pro Glu Lys Ala Asn Arg Thr Arg Ala
    450                 455                 460
Met Asp Asp Asp Ile Ala
465                 470
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<210> 5
<211> 1376
<212> DNA
<213> Anthozoa

<400> 5
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atgaggattc atgtcaccga aggggctcca ttaccatttg ccttcgacat tttggcaccg 180
tgttgtgagt acggcagcag gacctttgtc caccatacgg cagagattcc cgatttcttc 240

aagcagtctt tccctgaagg ctttacttgg gaaagaacca caacctatga agatggaggc 300
attcttactg ctcatcagga cacaagcctg gaggggaact gccttatata caaggtgaaa 360
gtccatggta ccaattttcc tgctgatggc cccgtgatga agaacaaatc aggaggatgg 420
gagccaagca ctgaggtggt ttatccagag aatggtgtcc tgtgtggacg taatgtgatg 480
gcccttaaag tcggtgatcg tcatttgatc tgccatcact atacttctta caggtccaag 540
aaagcagtcc gtgccttgac aatgccagga tttcatttta cagacatccg ccttcagatg 600
ctgaggaaaa agaaagacga gtactttgaa ctgtacgaag catctgtggc taggtacagt 660
gatcttcctg aaaaagcaaa agatctcccg ggatgtctgg tttgttgaaa gaaagtatgc 720
gcatcaagat gtacatggaa ggcacggtta atggccatta tttcaagtgt gaaggagagg 780
gagacggcaa cccatttgca ggtacgcaga gcatgaggat tcatgtcacc gaaggggctc 840
cattaccatt tgccttcgac attttggcac cgtgttgtga gtacggcagc aggacctttg 900
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<210> 6
<211> 458
<212> PRT
<213> Anthozoa

<400> 6
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Asn Pro Phe Ala Gly Thr Gln Ser Met Arg Ile His Val Thr Glu Gly
35 40 45
Ala Pro Leu Pro Phe Ala Phe Asp Ile Leu Ala Pro Cys Cys Glu Tyr
50 55 60
Gly Ser Arg Thr Phe Val His His Thr Ala Glu Ile Pro Asp Phe Phe
65 70 75 80
Lys Gln Ser Phe Pro Glu Gly Phe Thr Trp Glu Arg Thr Thr Thr Tyr
85 90 95
Glu Asp Gly Gly Ile Leu Thr Ala His Gln Asp Thr Ser Leu Glu Gly
100 105 110
Asn Cys Leu Ile Tyr Lys Val Lys Val His Gly Thr Asn Phe Pro Ala
115 120 125
Asp Gly Pro Val Met Lys Asn Lys Ser Gly Gly Trp Glu Pro Ser Thr
130 135 140
Glu Val Val Tyr Pro Glu Asn Gly Val Leu Cys Gly Arg Asn Val Met
145 150 155 160
Ala Leu Lys Val Gly Asp Arg His Leu Ile Cys His His Tyr Thr Ser
165 170 175
Tyr Arg Ser Lys Lys Ala Val Arg Ala Leu Thr Met Pro Gly Phe His
180 185 190
Phe Thr Asp Ile Arg Leu Gln Met Leu Arg Lys Lys Lys Asp Glu Tyr
195 200 205
Phe Glu Leu Tyr Glu Ala Ser Val Ala Arg Tyr Ser Asp Leu Pro Glu
210 215 220
Lys Ala Asn Arg Ser Pro Gly Met Ser Gly Leu Leu Lys Glu Ser Met
225 230 235 240
Arg Ile Lys Met Tyr Met Glu Gly Thr Val Asn Gly His Tyr Phe Lys
245 250 255
Cys Glu Gly Glu Gly Asp Gly Asn Pro Phe Ala Gly Thr Gln Ser Met

```
            260                 265                 270
Arg Ile His Val Thr Glu Gly Ala Pro Leu Pro Phe Ala Phe Asp Ile
        275                 280                 285
Leu Ala Pro Cys Cys Glu Tyr Gly Ser Arg Thr Phe Val His His Thr
    290                 295                 300
Ala Glu Ile Pro Asp Phe Phe Lys Gln Ser Phe Pro Glu Gly Phe Thr
305                 310                 315                 320
Trp Glu Arg Thr Thr Thr Tyr Glu Asp Gly Gly Ile Leu Thr Ala His
                325                 330                 335
Gln Asp Thr Ser Leu Glu Gly Asn Cys Leu Ile Tyr Lys Val Lys Val
            340                 345                 350
His Gly Thr Asn Phe Pro Ala Asp Gly Pro Val Met Lys Asn Lys Ser
        355                 360                 365
Gly Gly Trp Glu Pro Ser Thr Glu Val Val Tyr Pro Glu Asn Gly Val
    370                 375                 380
Leu Cys Gly Arg Asn Val Met Ala Leu Lys Val Gly Asp Arg His Leu
385                 390                 395                 400
Ile Cys His His Tyr Thr Ser Tyr Arg Ser Lys Lys Ala Val Arg Ala
                405                 410                 415
Leu Thr Met Pro Gly Phe His Phe Thr Asp Ile Arg Leu Gln Met Leu
            420                 425                 430
Arg Lys Lys Lys Asp Glu Tyr Phe Glu Leu Tyr Glu Ala Ser Val Ala
        435                 440                 445
Arg Tyr Ser Asp Leu Pro Glu Lys Ala Asn
    450                 455
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<210> 7
<211> 1404
<212> DNA
<213> anthozoa

<400> 7

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atgaagatcg aggtgatcga gggcggcccc ctgcccttcg ccttccacat cctgtccacc 180
tcctgcatgt acggctccaa ggccttcatc aagtacgtgt ccggcatccc cgactacttc 240
aagcagtccc tccccgaggg cttcacctgg gagcgcacca ccacctacga ggacggcggc 300
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gagccctcca ccgagatcgt gtacgaggtg gacggcgtgc tgcgcggcca gtccagcatg 480
gccctggagt gccccggcgg tcgccacctg acctgccacc tgcacaccac ctaccgctcc 540
aagaagcccg cctccgccct gaagatgccc ggcttccact tcgaggacca ccgcatcgag 600
atcctggagg aggtggagaa gggcaagtgc tacaagcagt acgaggccgc cgtgggccgc 660
tactgcgacg ccgccccctc caagctgggc cacaacagat ctcccgggat ggcctccctg 720
ctgaccgaga ccatgccctt caggaccacc atcgagggca ccgtgaacgg ccactacttc 780
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gagatcgtgt acgaggtgga cggcgtgctg cgcggccagt ccagcatggc cctggagtgc 1200
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<210> 8

<211> 468
<212> PRT
<213> Anthozoa

<400> 8

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            20                  25                  30
Asn Pro Leu Glu Gly Thr Gln Glu Met Lys Ile Glu Val Ile Glu Gly
        35                  40                  45
Gly Pro Leu Pro Phe Ala Phe His Ile Leu Ser Thr Ser Cys Met Tyr
    50                  55                  60
Gly Ser Lys Ala Phe Ile Lys Tyr Val Ser Gly Ile Pro Asp Tyr Phe
65                  70                  75                  80
Lys Gln Ser Leu Pro Glu Gly Phe Thr Trp Glu Arg Thr Thr Thr Tyr
                85                  90                  95
Glu Asp Gly Gly Phe Leu Thr Ala His Gln Asp Thr Ser Leu Asp Gly
            100                 105                 110
Asp Cys Leu Val Tyr Lys Val Lys Ile Leu Gly Asn Asn Phe Pro Ala
        115                 120                 125
Asp Gly Pro Val Met Gln Asn Lys Ala Gly Arg Trp Glu Pro Ser Thr
    130                 135                 140
Glu Ile Val Tyr Glu Val Asp Gly Val Leu Arg Gly Gln Ser Ser Met
145                 150                 155                 160
Ala Leu Glu Cys Pro Gly Gly Arg His Leu Thr Cys His Leu His Thr
                165                 170                 175
Thr Tyr Arg Ser Lys Lys Pro Ala Ser Ala Leu Lys Met Pro Gly Phe
            180                 185                 190
His Phe Glu Asp His Arg Ile Glu Ile Leu Glu Glu Val Glu Lys Gly
        195                 200                 205
Lys Cys Tyr Lys Gln Tyr Glu Ala Ala Val Gly Arg Tyr Cys Asp Ala
    210                 215                 220
Ala Pro Ser Lys Leu Gly His Asn Arg Ser Pro Gly Met Ala Ser Leu
225                 230                 235                 240
Leu Thr Glu Thr Met Pro Phe Arg Thr Thr Ile Glu Gly Thr Val Asn
                245                 250                 255
Gly His Tyr Phe Lys Cys Thr Gly Lys Gly Glu Gly Asn Pro Leu Glu
            260                 265                 270
Gly Thr Gln Glu Met Lys Ile Glu Val Ile Glu Gly Gly Pro Leu Pro
        275                 280                 285
Phe Ala Phe His Ile Leu Ser Thr Ser Cys Met Tyr Gly Ser Lys Ala
    290                 295                 300
Phe Ile Lys Tyr Val Ser Gly Ile Pro Asp Tyr Phe Lys Gln Ser Leu
305                 310                 315                 320
Pro Glu Gly Phe Thr Trp Glu Arg Thr Thr Thr Tyr Glu Asp Gly Gly
                325                 330                 335
Phe Leu Thr Ala His Gln Asp Thr Ser Leu Asp Gly Asp Cys Leu Val
            340                 345                 350
Tyr Lys Val Lys Ile Leu Gly Asn Asn Phe Pro Ala Asp Gly Pro Val
        355                 360                 365
Met Gln Asn Lys Ala Gly Arg Trp Glu Pro Ser Thr Glu Ile Val Tyr
    370                 375                 380
Glu Val Asp Gly Val Leu Arg Gly Gln Ser Ser Met Ala Leu Glu Cys
385                 390                 395                 400
Pro Gly Gly Arg His Leu Thr Cys His Leu His Thr Thr Tyr Arg Ser
                405                 410                 415
Lys Lys Pro Ala Ser Ala Leu Lys Met Pro Gly Phe His Phe Glu Asp
            420                 425                 430
```

```
His Arg Ile Glu Ile Leu Glu Glu Val Glu Lys Gly Lys Cys Tyr Lys
        435                 440                 445
Gln Tyr Glu Ala Ala Val Gly Arg Tyr Cys Asp Ala Ala Pro Ser Lys
    450                 455                 460
Leu Gly His Asn
465
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<210> 9
<211> 1398
<212> DNA
<213> Anthozoa

<400> 9

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aagatcgagg tgatcgaggg cggccccctg cccttcgcct tccacatcct gtccacctcc 180
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gagaccatgc ccttcaggac caccatcgag ggcaccgtga acggccacta cttcaagtgc 780
accggcaagg gcgagggcaa ccccctcgag ggcacccagg agatgaagat cgaggtgatc 840
gagggcggcc ccctgccctt cgccttccac atcctgtcca cctcctgcat gtacggctcc 900
aaggccttca tcaagtacgt gtccggcatc cccgactact tcaagcagtc cctccccgag 960
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<210> 10
<211> 466
<212> PRT
<213> Anthozoa

<400> 10

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Ala Ser Leu Leu Thr Glu Thr Met Pro Phe Arg Thr Thr Ile Glu Gly
 1               5                  10                  15
Thr Val Asn Gly His Tyr Phe Lys Cys Thr Gly Lys Gly Glu Gly Asn
            20                  25                  30
Pro Leu Glu Gly Thr Gln Glu Met Lys Ile Glu Val Ile Glu Gly Gly
        35                  40                  45
Pro Leu Pro Phe Ala Phe His Ile Leu Ser Thr Ser Cys Met Tyr Gly
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Ser Lys Ala Phe Ile Lys Tyr Val Ser Gly Ile Pro Asp Tyr Phe Lys
65                  70                  75                  80
Gln Ser Leu Pro Glu Gly Phe Thr Trp Glu Arg Thr Thr Thr Tyr Glu
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Asp Gly Gly Phe Leu Thr Ala His Gln Asp Thr Ser Leu Asp Gly Asp
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Cys Leu Val Tyr Lys Val Lys Ile Leu Gly Asn Asn Phe Pro Ala Asp
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Gly Pro Val Met Gln Asn Lys Ala Gly Arg Trp Glu Pro Ser Thr Glu
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Ile Val Tyr Glu Val Asp Gly Val Leu Arg Gly Gln Ser Leu Met Ala
145                 150                 155                 160
Leu Glu Cys Pro Gly Gly Arg His Leu Thr Cys His Leu His Thr Thr
                165                 170                 175
Tyr Arg Ser Lys Lys Pro Ala Ser Ala Leu Lys Met Pro Gly Phe His
            180                 185                 190
Phe Glu Asp His Arg Ile Glu Ile Leu Glu Glu Val Glu Lys Gly Lys
        195                 200                 205
Cys Tyr Lys Gln Tyr Glu Ala Ala Val Gly Arg Tyr Cys Asp Ala Ala
    210                 215                 220
Pro Ser Lys Leu Gly His Asn Arg Ser Pro Gly Ala Ser Leu Leu Thr
225                 230                 235                 240
Glu Thr Met Pro Phe Arg Thr Thr Ile Glu Gly Thr Val Asn Gly His
                245                 250                 255
Tyr Phe Lys Cys Thr Gly Lys Gly Glu Gly Asn Pro Leu Glu Gly Thr
            260                 265                 270
Gln Glu Met Lys Ile Glu Val Ile Glu Gly Gly Pro Leu Pro Phe Ala
        275                 280                 285
Phe His Ile Leu Ser Thr Ser Cys Met Tyr Gly Ser Lys Ala Phe Ile
    290                 295                 300
Lys Tyr Val Ser Gly Ile Pro Asp Tyr Phe Lys Gln Ser Leu Pro Glu
305                 310                 315                 320
Gly Phe Thr Trp Glu Arg Thr Thr Thr Tyr Glu Asp Gly Gly Phe Leu
                325                 330                 335
Thr Ala His Gln Asp Thr Ser Leu Asp Gly Asp Cys Leu Val Tyr Lys
            340                 345                 350
Val Lys Ile Leu Gly Asn Asn Phe Pro Ala Asp Gly Pro Val Met Gln
        355                 360                 365
Asn Lys Ala Gly Arg Trp Glu Pro Ser Thr Glu Ile Val Tyr Glu Val
    370                 375                 380
Asp Gly Val Leu Arg Gly Gln Ser Leu Met Ala Leu Glu Cys Pro Gly
385                 390                 395                 400
Gly Arg His Leu Thr Cys His Leu His Thr Thr Tyr Arg Ser Lys Lys
                405                 410                 415
Pro Ala Ser Ala Leu Lys Met Pro Gly Phe His Phe Glu Asp His Arg
            420                 425                 430
Ile Glu Ile Leu Glu Glu Val Glu Lys Gly Lys Cys Tyr Lys Gln Tyr
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His Asn
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